RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
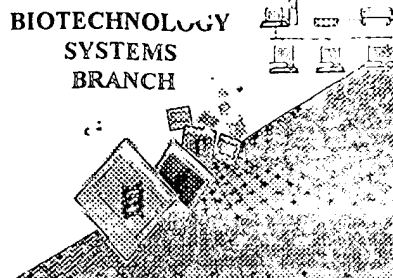BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/654, 281_

Source: _1642_   BEST AVAILABLE COPY

Date Processed by STIC: _3/16/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION**   SERIAL NUMBER: _O 9/654,281_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ✓ Variable Length
Sequence(s) _1_ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

1642

```
       RAW SEQUENCE LISTING                 DATE: 03/16/2001
       PATENT APPLICATION:  US/09/654,281   TIME: 15:13:59

       Input Set : A:\PTO.txt
       Output Set: N:\CRF3\03162001\I654281.raw
```

Does Not Comply
Corrected Diskette Needed

pp 1-2,5

```
 3 <110> APPLICANT: Sedivy, John
 4         Kolch, Walter
 5         Yeung, Kam Chi
 7 <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and Modulation
 8         of Cell Proliferation and Growth
10 <130> FILE REFERENCE: 3564/1010
12 <140> CURRENT APPLICATION NUMBER: 09/654,281
13 <141> CURRENT FILING DATE: 2000-09-01
15 <150> PRIOR APPLICATION NUMBER: 60/151,992
16 <151> PRIOR FILING DATE: 1999-09-01
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 42
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial/Unknown
27 <220> FEATURE:
28 <221> NAME/KEY: UNSURE
29 <222> LOCATION: (3)..(5)
30 <223> OTHER INFORMATION: X = any amino acid
33 <220> FEATURE:
34 <221> NAME/KEY: UNSURE
35 <222> LOCATION: (9)..(9)
36 <223> OTHER INFORMATION: Z = a hydrophobic amino acid residue
39 <220> FEATURE:
40 <221> NAME/KEY: UNSURE
41 <222> LOCATION: (11)..(13)
42 <223> OTHER INFORMATION: X = any amino acid
45 <220> FEATURE:
46 <221> NAME/KEY: UNSURE
47 <222> LOCATION: (14)..(14)
48 <223> OTHER INFORMATION: B = a negatively charged amino acid residue
51 <220> FEATURE:
52 <221> NAME/KEY: UNSURE
53 <222> LOCATION: (15)..(18)
54 <223> OTHER INFORMATION: X = any amino acid residue
57 <220> FEATURE:
58 <221> NAME/KEY: UNSURE
59 <222> LOCATION: (20)..(21)
60 <223> OTHER INFORMATION: X = any amino acid residue
63 <220> FEATURE:
64 <221> NAME/KEY: UNSURE
65 <222> LOCATION: (23)..(23)
66 <223> OTHER INFORMATION: X = between 10 and 50 of any amino acid residue
69 <220> FEATURE:
70 <221> NAME/KEY: UNSURE
71 <222> LOCATION: (25)..(28)
```

[handwritten annotations:]
) please correct this error, it appears in subsequent sequences

invalid – per 1.823 of new Sequence Rules, the only valid <213> responses are: Unknown or Artificial Sequence or scientific name (Genus/species) (one of the three)

Xaa
X = (circled)
delete
Z = (circled) don't use this – just show "Z"
Xaa
X = (circled)
delete
Xaa
X = (circled)
Xaa
X = (circled)
Xaa
X = (circled)

also, see item 12 on Error Summary Sheet

variable length not permitted – see item 6 on Error Summary Sheet

RAW SEQUENCE LISTING   DATE: 03/16/2001
PATENT APPLICATION: US/09/654,281   TIME: 15:13:59

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw

Xaa
72 <223> OTHER INFORMATION: (X) = any amino acid residue
75 <220> FEATURE:
76 <221> NAME/KEY: UNSURE
77 <222> LOCATION: (30)..(30) *Xaa*
78 <223> OTHER INFORMATION: (X) = between 2 and 4 of any amino acid residue   *see item 6 on Erra Summary Sheet*
81 <220> FEATURE:
82 <221> NAME/KEY: UNSURE
83 <222> LOCATION: (32)..(32) *Xaa*
84 <223> OTHER INFORMATION: (X) = any amino acid residue
87 <220> FEATURE:
88 <221> NAME/KEY: UNSURE
89 <222> LOCATION: (35)..(35) *Xaa*
90 <223> OTHER INFORMATION: (X) = an aromatic amino acid residue
93 <220> FEATURE:
94 <221> NAME/KEY: UNSURE
95 <222> LOCATION: (37)..(37) *Xaa*
96 <223> OTHER INFORMATION: (X) = any amino acid residue
99 <220> FEATURE:
100 <221> NAME/KEY: UNSURE   *delete*
101 <222> LOCATION: (38)..(38)
102 <223> OTHER INFORMATION: (Z =) a hydrophobic amino acid residue
105 <220> FEATURE:
106 <221> NAME/KEY: UNSURE
107 <222> LOCATION: (39)..(41) *Xaa*
108 <223> OTHER INFORMATION: (X) = any amino acid residue
111 <400> SEQUENCE: 1
W--> 113 Thr Leu Xaa Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
114 1   5   10   15
W--> 116 Xaa Xaa Glu Xaa Xaa His Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Gly Xaa
117   20   25   30
W--> 119 His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
120   35   40
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 187
124 <212> TYPE: PRT
125 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 2
129 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
130 1   5   10   15
132 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
133   20   25   30
135 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
136   35   40   45
138 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
139   50   55   60
141 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
142 65   70   75   80
144 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
145   85   90   95

RAW SEQUENCE LISTING   DATE: 03/16/2001
PATENT APPLICATION: US/09/654,281   TIME: 15:13:59

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw

```
147 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
148             100             105             110
150 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
151         115             120             125
153 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
154     130             135             140
156 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
157 145             150             155             160
159 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
160             165             170             175
162 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
163             180             185
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 187
167 <212> TYPE: PRT
168 <213> ORGANISM: Mus musculus
170 <220> FEATURE:
171 <221> NAME/KEY: UNSURE
172 <222> LOCATION: (150)..(150)
173 <223> OTHER INFORMATION: X = any amino acid residue
176 <400> SEQUENCE: 3
178 Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
179 1               5               10              15
181 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
182             20              25              30
184 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
185         35              40              45
187 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
188     50              55              60
190 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
191 65              70              75              80
193 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
194             85              90              95
196 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
197             100             105             110
199 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
200         115             120             125
202 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
203     130             135             140
205 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
206 145             150             155             160
208 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
209             165             170             175
211 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
212             180             185
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 187
216 <212> TYPE: PRT
217 <213> ORGANISM: Drosophila
```

RAW SEQUENCE LISTING   DATE: 03/16/2001
PATENT APPLICATION: US/09/654,281   TIME: 15:13:59

        Input Set : A:\PTO.txt
        Output Set: N:\CRF3\03162001\I654281.raw

219 <400> SEQUENCE: 4
221 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
222 1   5   10   15
224 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
225   20   25   30
227 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
228   35   40   45
230 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
231   50   55   60
233 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
234 65   70   75   80
236 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
237   85   90   95
239 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
240   100   105   110
242 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
243   115   120   125
245 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
246   130   135   140
248 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
249 145   150   155   160
251 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
252   165   170   175
254 Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys
255   180   185
257 <210> SEQ ID NO: 5
258 <211> LENGTH: 220
259 <212> TYPE: PRT
260 <213> ORGANISM: C. elegans
262 <400> SEQUENCE: 5
264 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
265 1   5   10   15
267 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
268   20   25   30
270 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
271   35   40   45
273 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys
274   50   55   60
276 Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
277 65   70   75   80
279 Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
280   85   90   95
282 Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
283   100   105   110
285 Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
286   115   120   125
288 Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
289   130   135   140
291 Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln

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RAW SEQUENCE LISTING              DATE: 03/16/2001
PATENT APPLICATION:  US/09/654,281    TIME: 15:13:59

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw
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```
292 145                  150                 155                 160
294 Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser
295              165                 170                 175
297 Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His
298          180                 185                 190
300 Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp
301          195                 200                 205
303 Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala
304      210                 215                 220
306 <210> SEQ ID NO: 6
307 <211> LENGTH: 181
308 <212> TYPE: PRT
309 <213> ORGANISM: Antirrhinum-CEN
311 <400> SEQUENCE: 6
313 Met Ala Ala Lys Val Ser Ser Asp Pro Leu Val Ile Gly Arg Val Ile
314 1               5                  10                  15
316 Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile
317          20                 25                  30
319 Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu
320          35                 40                  45
322 Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly
323      50                 55                  60
325 Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro
326 65                 70                 75                  80
328 Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr
329              85                 90                  95
331 Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser
332          100                105                 110
334 Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu
335          115                120                 125
337 Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val
338      130                135                 140
340 Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu
341 145                150                155                 160
343 Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr
344              165                170                 175
346 Ala Ala Arg Arg Arg
347              180
349 <210> SEQ ID NO: 7
350 <211> LENGTH: 176
351 <212> TYPE: PRT
352 <213> ORGANISM: Aradopsis-TFL1
354 <400> SEQUENCE: 7
356 Met Glu Asn Met Gly Thr Arg Val Ile Glu Pro Leu Ile Met Gly Arg
357 1               5                  10                  15
359 Val Val Gly Asp Val Leu Asp Phe Phe Thr Pro Thr Thr Lys Met Asn
360          20                 25                  30
362 Val Ser Tyr Asn Lys Lys Gln Val Asn Gly His Glu Leu Phe Pro Ser
363          35                 40                  45
```

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 03/16/2001
PATENT APPLICATION: US/09/654,281   TIME: 15:14:00

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw

L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10